

SEQUENCE LISTING

<110> Seoul National University Industry Foundation

<120> ROOT-SPECIFIC EXPASIN GENE REGULATING ROOT GROWTH
AND OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT

<130> OP03-0015

<150> KR 2003-19069

<151> 2003-03-27

<160> 9

<170> KopatentIn 1.71

<210> 1

<211> 1089

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (52)..(816)

<223> Glycine max expansin (GmEXP1)

<400> 1

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atg ggc aaa atc atg ctt gtt ttg ggt agc ctc att gga tta tgc tgt 99

Met Gly Lys Ile Met Leu Val Leu Gly Ser Leu Ile Gly Leu Cys Cys

1 5 10 15

ttc aca atc act acc tat gcc ttc tca cct tct gga tgg acc aac gcc 147

Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala

20 25 30

cat gcc act ttt tat ggg ggt agt gat gct tca gga act atg ggg gga 195

His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly

35 40 45

gct tgt ggg tat ggg aat ctg tat gca act ggg tat gga act aga act 243

Ala Cys Gly Tyr Gly Asn Leu Tyr Ala Thr Gly Tyr Gly Thr Arg Thr

50 55 60

gca gct tta agc act gcc tta ttt aat gat gga gct tcc tgt ggt cag 291

Ala Ala Leu Ser Thr Ala Leu Phe Asn Asp Gly Ala Ser Cys Gly Gln

65 70 75 80

tgc tac aaa att ata tgt gat tac aaa tca gac tct aga tgg tgc atc 339

Cys Tyr Lys Ile Ile Cys Asp Tyr Lys Ser Asp Ser Arg Trp Cys Ile

85 90 95

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aaa gga aga tct gta acc gta act gcc aca aac ttt tgc cct ccc aat 387
Lys Gly Arg Ser Val Thr Val Thr Ala Thr Asn Phe Cys Pro Pro Asn
      100      105      110
ttc gcc ctt cct aac aac aat gga ggc tgg tgc aac cca cca ctc aag 435
Phe Ala Leu Pro Asn Asn Asn Gly Gly Trp Cys Asn Pro Pro Leu Lys
      115      120      125
cat ttt gat atg gcc caa ccc gct tgg gaa aag att ggt att tac aga 483
His Phe Asp Met Ala Gln Pro Ala Trp Glu Lys Ile Gly Ile Tyr Arg
      130      135      140
gga ggg atc gtc ccc gtg cta ttt caa agg gtt cca tgc aaa aag cat 531
Gly Gly Ile Val Pro Val Leu Phe Gln Arg Val Pro Cys Lys Lys His
      145      150      155      160
gga ggg gtt agg ttc agt gtg aat ggg agg gac tac ttt gag cta gta 579
Gly Gly Val Arg Phe Ser Val Asn Gly Arg Asp Tyr Phe Glu Leu Val
      165      170      175
ttg atc agc aat gtg ggg ggt gct gga tcc atc caa tca gtg ttc att 627
Leu Ile Ser Asn Val Gly Gly Ala Gly Ser Ile Gln Ser Val Phe Ile
      180      185      190
aaa ggc tca aaa act gga tgg atg gca atg tca aga aat tgg ggt tct 675
Lys Gly Ser Lys Thr Gly Trp Met Ala Met Ser Arg Asn Trp Gly Ser
      195      200      205
aat tgg caa tcc aat gcg tat ttg aat ggt caa tct ttg tcc ttc agg 723
Asn Trp Gln Ser Asn Ala Tyr Leu Asn Gly Gln Ser Leu Ser Phe Arg
      210      215      220
gtc acc acc act gat gga gag acc aga gtt ttc caa gat att gtt cca 771
Val Thr Thr Thr Asp Gly Glu Thr Arg Val Phe Gln Asp Ile Val Pro
      225      230      235      240
gta agt tgg aca ttc ggc caa act ttc tct agc cca gtt cag ttc taag 820
Val Ser Trp Thr Phe Gly Gln Thr Phe Ser Ser Pro Val Gln Phe
      245      250      255
ctgattacag ataaaccaac caacggctga ggcgtgcttt tttattttat tactggagct 880
gccccccacc cttcttctgg ttttgattat tcccatcaac tccaagccct ctatcaaggc 940
ataaattctt atcaataata caatcaatca ccatcatatc atcataagct tgtatatcaa 1000
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tgaagttcaa aaaaaaaaaa aaaaaaaaaa 1089

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<210> 2
<211> 255
<212> PRT
<213> Glycine max

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<400> 2
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Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
      20           25           30
His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly
      35           40           45
Ala Cys Gly Tyr Gly Asn Leu Tyr Ala Thr Gly Tyr Gly Thr Arg Thr

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50 55 60
 Ala Ala Leu Ser Thr Ala Leu Phe Asn Asp Gly Ala Ser Cys Gly Gln
 65 70 75 80
 Cys Tyr Lys Ile Ile Cys Asp Tyr Lys Ser Asp Ser Arg Trp Cys Ile
 85 90 95
 Lys Gly Arg Ser Val Thr Val Thr Ala Thr Asn Phe Cys Pro Pro Asn
 100 105 110
 Phe Ala Leu Pro Asn Asn Asn Gly Gly Trp Cys Asn Pro Pro Leu Lys
 115 120 125
 His Phe Asp Met Ala Gln Pro Ala Trp Glu Lys Ile Gly Ile Tyr Arg
 130 135 140
 Gly Gly Ile Val Pro Val Leu Phe Gln Arg Val Pro Cys Lys Lys His
 145 150 155 160
 Gly Gly Val Arg Phe Ser Val Asn Gly Arg Asp Tyr Phe Glu Leu Val
 165 170 175
 Leu Ile Ser Asn Val Gly Gly Ala Gly Ser Ile Gln Ser Val Phe Ile
 180 185 190
 Lys Gly Ser Lys Thr Gly Trp Met Ala Met Ser Arg Asn Trp Gly Ser
 195 200 205
 Asn Trp Gln Ser Asn Ala Tyr Leu Asn Gly Gln Ser Leu Ser Phe Arg
 210 215 220
 Val Thr Thr Thr Asp Gly Glu Thr Arg Val Phe Gln Asp Ile Val Pro
 225 230 235 240
 Val Ser Trp Thr Phe Gly Gln Thr Phe Ser Ser Pro Val Gln Phe
 245 250 255

<210> 3
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 3
 nnggatccga ygcntcnggn acnatgggyg gygctgygt angg

44

<210> 4
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 4

<210> 5
 <211> 519
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Probe

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 ggnacnmgna cngcngcnyt nwsnacngcn ynttyaayg ayggngcnws ntgyggncar 120
 tgytayaara thattgyga ytayaarwsn gaywsnmgt ggtgyathaa rggnmgnwsn 180
 gtnacngtna cngcnacnaa yttygyccn ccnaaytgy cnytnccnaa yaayaayggn 240
 ggntgggtgya ayccncnnyt naarcaytty gayatggcnc arccngcntg ggaraarath 300
 ggnathtaym gnggnggnat hgtncngtn ynttycarm gngtnccntg yaaraarcay 360
 gnggnggtm gnttywsngt naayggnmgn gaytaytgy aryngtnyt nathwsnaay 420
 gtnggngng cnggnwsnat hcarwsngtn ttyathaarg gnwsnaarac nggntggatg 480
 gcnatgwsnm gnaaytggg nwsnaaytgg carwsnaay 519

<210> 6
 <211> 269
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> RNA probe(antisense)

<400> 6
 aauaaaauaa aaaagcacgc cucagccguu gguugguuuu ucuguaauca gcuuagaacu 60
 gaacugggcu agagaaaguu uggccgaaug uccaacuuac uggaacaaua ucuuggaaaa 120
 cucuggucuc uccaucagug guggugaccc ugaaggacaa agauugacca uucaaaucg 180
 cauuggauug ccaauuagaa cccaauuuc uugacauugc cauccauca guuuuugagc 240
 cuuuaaugaa cacugauugg auggauca 269

<210> 7
 <211> 389
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> RNA probe(sense)

<400> 7
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 aaauuggggg ucuaauuggc aauccaauugc guauuugaau ggucaauucu uguccuucag 120
 ggucaccacc acugauggag agaccagagu uuuccaagau auuguuccag uaaguuggac 180
 auucggccaa acuuucucua gcccaguuca guucuaagcu gauuacagau aaaccaacca 240
 acggcugagg cgugcuuuuu uauuuuauua cuggagcugc ccgccacccu ucuucugguu 300
 uugauuauuc ccaucaacuc caagcccucu aucaaggcau aaauucuuau caauauaca 360
 aucaaucacc aucauaucau cauaagcuu 389

<210> 8
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 8
 accaagcttc aacctctcat cattaggc 28

<210> 9
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 9
 accaagcttg gagttgatgg gaataatca 29